

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company
<120> Plant Glutamine Amidotransferase Homologs
<130> BB1129
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<150> 60/107,275
<151> 1998-11-05
<160> 15
<170> Microsoft Office 97
<210> 1
<211> 1956
<212> DNA
<213> Impatiens balsamia

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<210> 2
<211> 558

<212> PRT

<213> Impatiens balsamia

<400> 2

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 20 25 30
 Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn Ala Ile Arg Thr
 35 40 45
 Leu Gly Phe Asp Ile Lys Asp Val Gln Lys Pro Glu Asp Ile Leu Asn
 50 55 60
 Ala Lys Arg Leu Ile Phe Pro Gly Val Gly Ala Phe Ala Pro Ala Met
 65 70 75 80
 Asp Val Leu Ile Arg Lys Gly Leu Ala Glu Ala Leu Cys Thr Tyr Ile
 85 90 95
 Gln Asn Asp Arg Pro Phe Leu Gly Ile Cys Leu Gly Leu Gln Leu Leu
 100 105 110
 Phe Glu Ser Ser Glu Glu Asn Gly Pro Ile Gln Gly Leu Gly Leu Ile
 115 120 125
 Pro Gly Arg Val Gly Arg Phe Glu Ser Ser Asn Gly Leu Arg Val Pro
 130 135 140
 His Ile Gly Trp His Ala Leu Asp Ile Lys Glu Gly Ser Ala Ile Leu
 145 150 155 160
 Asp Asp Val Gly Asn Gln His Val Tyr Phe Val His Ser Tyr Arg Ala
 165 170 175
 Asn Ala Glu Asp Asn Lys Glu Trp Ile Ser Ser Thr Cys Ser Tyr Gly
 180 185 190
 Asp Asp Phe Ile Ala Ser Ile Gln Lys Gly Asn Val His Ala Val Gln
 195 200 205
 Phe His Pro Glu Lys Ser Gly Gly Val Gly Leu Ser Ile Leu Arg Arg
 210 215 220
 Phe Leu Asn Ala Asp Ser Phe Asn Asn Lys Arg Gln Lys Pro Met Asn
 225 230 235 240
 Gly Lys Ala Ser Lys Leu Ala Lys Arg Val Ile Ala Cys Leu Asp Val
 245 250 255
 Arg Ala Asn Asp Asn Gly Asp Leu Val Val Thr Lys Gly Asp Gln Tyr
 260 265 270
 Asp Val Arg Glu Arg Thr Glu Glu Asn Glu Val Arg Asn Leu Gly Lys
 275 280 285
 Pro Val Glu Leu Ala Gly Gln Tyr Tyr Leu Asp Gly Ala Asp Glu Val
 290 295 300

Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly Asp Leu
 305 310 315 320
 Pro Met Leu Gln Val Leu Gln Arg Ala Ser Glu Asn Val Phe Val Pro
 325 330 335
 Leu Thr Val Gly Gly Gly Ile Arg Asp Phe Thr Asp Ala Asn Gly Arg
 340 345 350
 Tyr Tyr Ser Ser Leu Glu Val Ala Ser Glu Tyr Phe Arg Ser Gly Ala
 355 360 365
 Asp Lys Val Ser Ile Gly Ser Asp Ala Val Tyr Thr Ala Glu Glu Tyr
 370 375 380
 Ile Lys Thr Gly Val Lys Thr Gly Lys Ser Ser Ile Glu Gln Ile Ser
 385 390 395 400
 Thr Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro Arg Arg
 405 410 415
 Val Tyr Leu Arg Lys Pro Asp Glu Val Glu Phe Lys Ala Ile Lys Val
 420 425 430
 Ser His Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln Cys Thr
 435 440 445
 Val Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala
 450 455 460
 Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile
 465 470 475 480
 Asp Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Ile Lys Leu
 485 490 495
 Ile Ser Asp Ala Val Asn Ile Pro Val Ile Ala Ser Ser Gly Ala Gly
 500 505 510
 Val Ala Asp His Phe Ser Glu Val Phe Asn Glu Thr Asn Ala Ser Ala
 515 520 525
 Ala Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Lys Ala
 530 535 540
 Val Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Leu
 545 550 555

<210> 3
 <211> 587
 <212> DNA
 <213> Zea mays

<220>
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 ggctccttca tcgcctgctc cagcgtgcct gcgtgacata agcgtcgatt gattggcgag 180
 aaaggggacg aatgcagccg ccgttgacag cgcaggagc aatggctaac gtcgccgcta 240
 tcctcaccgt cccctgctcc gcgggccgcc gcccgaaagc gagcaaccag ccccgcggat 300
 gcggtccgt ctccgtctcc gtctccgtcc gtgcgtcctc cggcgcaaac acggtgactc 360
 tgctggacta cggcgcgggg aacgtacgca gcgtgcgcaa cgcaattcgc tacctcggct 420
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 cccggtgtcg gcgnttcgg ctccgccatg gacgtccnca ccaggacggg catgccaaacg 540
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<210> 4
 <211> 130
 <212> PRT
 <213> Zea mays

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 <222> (90)

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 Ile Leu Thr Val Pro Cys Ser Ala Gly Arg Arg Pro Lys Arg Ser Asn
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 Gln Pro Arg Gly Cys Gly Ser Val Ser Val Ser Val Ser Val Arg Ala
 35 40 45

Ser Ser Gly Ala Asn Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn
50 55 60

Val Arg Ser Val Arg Asn Ala Ile Arg Tyr Leu Gly Phe Asp Ile Arg
65 70 75 80

Asp Val Gln Ser Pro Glu Asp Ile Val Xaa Ala Glu Xaa Val Val Phe
85 90 95

Pro Gly Val Gly Ala Phe Gly Ser Ala Met Asp Val Xaa Thr Arg Thr
100 105 110

Gly Met Xaa Asn Ala Leu Arg Glu Tyr Ile Gln Arg Glu Arg Pro Phe
115 120 125

Xaa Gly
130

<210> 5
<211> 1084
<212> DNA
<213> Zea mays

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ggtcagcttc ttgaatataa ctggtttccg tgactttcca ttgggtgatt tgccaatgct 180
agaggtactg cgttgtgcct ctgaaaagg ttttgtgcca cttacagttg gtgggggcat 240
acgagacttc acagatgcaa atggaagata ctactcaagt ttggaggtag catcagaata 300
tttcagggtcc ggtgctgaca aaatttcaat tggaagtgat gctgtttatg ctgctgaagc 360
ctttttacag actggtgtaa agacagggaa aagcagcttg gagcaaactc cttagatata 420
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agcgaagct gtggaagaat tgggcgcagg agaaatactt cttaactgca ttgattgtga 660
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aaaa 1084

<210> 6
<211> 295
<212> PRT
<213> Zea mays

<400> 6
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1 5 10 15

Ser Lys Glu Val Arg Asn Leu Gly Lys Pro Val Asp Leu Ala Ser Gln
20 25 30

Tyr Tyr Ile Asp Gly Ala Asp Glu Val Ser Phe Leu Asn Ile Thr Gly
35 40 45

Phe Arg Asp Phe Pro Leu Gly Asp Leu Pro Met Leu Glu Val Leu Arg
 50 55 60
 Cys Ala Ser Glu Lys Val Phe Val Pro Leu Thr Val Gly Gly Gly Ile
 65 70 75 80
 Arg Asp Phe Thr Asp Ala Asn Gly Arg Tyr Tyr Ser Ser Leu Glu Val
 85 90 95
 Ala Ser Glu Tyr Phe Arg Ser Gly Ala Asp Lys Ile Ser Ile Gly Ser
 100 105 110
 Asp Ala Val Tyr Ala Ala Glu Ala Phe Leu Gln Thr Gly Val Lys Thr
 115 120 125
 Gly Lys Ser Ser Leu Glu Gln Ile Ser Arg Val Tyr Gly Asn Gln Ala
 130 135 140
 Val Val Val Ser Ile Asp Pro Arg Arg Val Tyr Val Lys Ser Gln Glu
 145 150 155 160
 Asp Val Pro Phe Lys Thr Val Lys Val Ser Thr Lys Gly Pro Ser Gly
 165 170 175
 Glu Glu Tyr Ala Trp Tyr Gln Cys Thr Val Asn Gly Gly Arg Asp Ser
 180 185 190
 Arg Ala Ile Gly Ala Tyr Glu Leu Ala Lys Ala Val Glu Glu Leu Gly
 195 200 205
 Ala Gly Glu Ile Leu Leu Asn Cys Ile Asp Cys Asp Gly Gln Gly Cys
 210 215 220
 Gly Phe Asp Ile Asp Leu Val Lys Met Val Ser Asp Ala Val Thr Ile
 225 230 235 240
 Pro Val Ile Ala Ser Ser Gly Ala Gly Ala Val Gln His Phe Ser Glu
 245 250 255
 Ile Phe Glu Lys Thr Asn Ala Ser Ala Ala Leu Ala Ala Gly Ile Phe
 260 265 270
 His Arg Lys Glu Val Pro Ile Leu Ala Val Lys Glu His Leu Val Asn
 275 280 285
 Ala Gly Val Glu Val Arg Val
 290 295

<210> 7
 <211> 494
 <212> DNA
 <213> Zea mays

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 gcctcggtct ccagctgctc ttcggattcc agcnnggaga nanggnccgt gtgagcggac 180
 tcggtgtgat atcaggcgtg gncaggcgat tcganticctc aaatggcctc atagtccac 240
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 gccagnatgt gtacttttgn tcactcctac cgcgtactgg cttcanngtg ctagtnagga 360
 aactgggggt tcctccatat ggcaactatg ggngacagct tttaatcctc catctcaa 420
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<210> 8
 <211> 86
 <212> PRT
 <213> Zea mays

<220>
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 <222> (23)

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 Leu Leu Phe Gly Phe Gln Xaa Gly Xaa Xaa Xaa Arg Val Ser Gly Leu
 20 25 30
 Gly Val Ile Ser Gly Val Xaa Arg Arg Phe Xaa Ser Ser Asn Gly Leu
 35 40 45
 Ile Val Pro His Val Gly Trp Asn Ala Leu Gln Xaa Thr Xaa Xaa Xaa
 50 55 60
 Pro Leu Leu Gln Gly Ala Asp Gly Gln Xaa Val Tyr Phe Xaa His Ser
 65 70 75 80
 Tyr Arg Val Leu Ala Ser
 85

<210> 9
 <211> 495
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (125)

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 gcgnggcctc tacggtcgcc gtgcgcgcgt ccggcgacgc tagcaccgtg acgctgctgg 180
 actacggcgc gggcaacgtg cgcagcgtgc gcaatgccat ccgccacctc ggtttcggca 240
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 tcggcgcctt cgggntcaag ccatggacgt cctcaaccgc ctccgggatg ggcggacgcg 360
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 gggcttgggg tntnt 495

<210> 10
 <211> 87
 <212> PRT
 <213> Oryza sativa

<220>

<221> UNSURE

<222> (72)

<400> 10

Met Val Ala Ala Thr Ser Ile Asn Ala Val Pro Cys Ser Ala Gly Arg
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Pro Lys Arg Arg Ser Gln Arg Arg Gly Ala Ser Thr Val Ala Val Arg
 20 25 30

Ala Ser Gly Asp Ala Ser Thr Val Thr Leu Leu Asp Tyr Gly Ala Gly
 35 40 45

Asn Val Arg Ser Val Arg Asn Ala Ile Arg His Leu Gly Phe Gly Ile
 50 55 60

Arg Asp Val Arg Ser Pro Glu Xaa Ile Leu Ala Ala Asp Arg Leu Val
 65 70 75 80

Phe Pro Gly Val Gly Ala Phe
 85

<210> 11

<211> 178

<212> DNA

<213> Glycine max

<400> 11

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 tcctcggtt tgacataaaa gatgtgcaaa ctccgcaaga tattctgaat gcaagtcggt 120
 tagtttttcc tgggtgttga gcatttgctg ctgccatga ggtgttaagc aaaactgg 178

<210> 12

<211> 58

<212> PRT

<213> Glycine max

<400> 12

Val Thr Leu Leu Asp Tyr Gly Ala Gly Asn Val Arg Ser Val Arg Asn
 1 5 10 15

Ala Ile Arg Phe Leu Gly Phe Asp Ile Lys Asp Val Gln Thr Pro Gln
 20 25 30

Asp Ile Leu Asn Ala Ser Arg Leu Val Phe Pro Gly Val Gly Ala Phe
 35 40 45

Ala Ala Ala Met Glu Val Leu Ser Lys Thr
 50 55

<210> 13

<211> 671

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (276)

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aattgggtgct tatgaactag caaaagcagt tgaagagctt ggtgctggtg aaatactact 180
taattgcatt gattgcgacg gtcaagggaa aggatttgat gtagatttaa ttaagttgat 240
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ctctgaggtg ttctataaaa caaatgcatac agcagcactt gctgctggca tttttcacag 360
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ttgtacgtta tccctttttg tgtaatctaa cgaagctctc aaaatgtcaa ccttttggat 540
catgaaaaga ttttcacaac gagacctttc ctttgtaata tttttaagga aaatatattt 600
accatgtgca gcactatctc tgaacatttg ttattacaaa attatttcat gtgtcaaaaa 660
aaaaaaaaa a 671

<210> 14
<211> 141
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (92)

<400> 14
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Asn Gly Gly Arg Glu Gly Arg Pro Ile Gly Ala Tyr Glu Leu Ala Lys
35 40 45
Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn Cys Ile Asp
50 55 60
Cys Asp Gly Gln Gly Lys Gly Phe Asp Val Asp Leu Ile Lys Leu Ile
65 70 75 80
Ser Asn Ala Val Ser Ile Pro Val Ile Ala Ser Xaa Gly Ala Gly Ala
85 90 95
Pro Glu His Phe Ser Glu Val Phe Tyr Lys Thr Asn Ala Ser Ala Ala
100 105 110
Leu Ala Ala Gly Ile Phe His Arg Lys Glu Val Pro Ile Gln Ser Val
115 120 125
Lys Glu His Leu Leu Lys Glu Gly Ile Glu Val Arg Ile
130 135 140

<210> 15
<211> 593
<212> PRT
<213> Arabidopsis thaliana

<400> 15
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1 5 10 15

Asn	Phe	Ser	Ser	Ser	Ser	Ile	Arg	Ala	Ser	Ser	Pro	Ala	Ser	Leu	
			20				25				30				
Phe	Leu	Ser	Gln	Lys	Ser	Ile	Gly	Asn	Val	Asn	Arg	Lys	Phe	Lys	Ser
		35					40					45			
Pro	Arg	Ser	Leu	Ser	Val	Arg	Ala	Ser	Ser	Thr	Ser	Asp	Ser	Val	Val
	50					55					60				
Thr	Leu	Leu	Asp	Tyr	Gly	Ala	Gly	Asn	Val	Arg	Ser	Ile	Arg	Asn	Ala
65					70					75					80
Leu	Arg	His	Leu	Gly	Phe	Ser	Ile	Lys	Asp	Val	Gln	Thr	Pro	Gly	Asp
				85					90					95	
Ile	Leu	Asn	Ala	Asp	Arg	Leu	Ile	Phe	Pro	Gly	Val	Gly	Pro	Phe	Ala
			100					105					110		
Pro	Ala	Met	Asp	Val	Leu	Asn	Arg	Thr	Gly	Met	Ala	Glu	Ala	Leu	Cys
		115					120					125			
Lys	Tyr	Ile	Glu	Asn	Asp	Arg	Pro	Phe	Leu	Gly	Ile	Cys	Leu	Gly	Leu
	130					135					140				
Gln	Leu	Leu	Phe	Asp	Ser	Ser	Glu	Gln	Asn	Gly	Pro	Val	Lys	Gly	Leu
145					150					155					160
Gly	Val	Ile	Pro	Gly	Ile	Val	Gly	Arg	Phe	Asp	Ala	Ser	Ala	Gly	Ile
				165					170					175	
Arg	Val	Pro	His	Ile	Gly	Trp	Asn	Ala	Leu	Gln	Val	Gly	Lys	Asp	Ser
			180					185					190		
Glu	Ile	Leu	Asp	Asp	Val	Gly	Asn	Arg	His	Val	Tyr	Phe	Val	His	Ser
		195					200					205			
Tyr	Arg	Ala	Ile	Pro	Ser	Asp	Glu	Asn	Lys	Asp	Trp	Ile	Ser	Ser	Thr
	210					215					220				
Cys	Asn	Tyr	Gly	Glu	Ser	Phe	Ile	Ser	Ser	Ile	Arg	Arg	Gly	Asn	Val
225					230					235					240
His	Ala	Val	Gln	Phe	His	Pro	Glu	Lys	Ser	Gly	Glu	Val	Gly	Leu	Ser
				245					250					255	
Val	Leu	Arg	Arg	Phe	Leu	His	Pro	Lys	Leu	Pro	Ala	Thr	Gln	Lys	Pro
			260					265					270		
Met	Glu	Gly	Lys	Ala	Ser	Lys	Leu	Ala	Lys	Arg	Val	Ile	Ala	Cys	Leu
		275					280					285			
Asp	Val	Arg	Thr	Asn	Asp	Lys	Gly	Asp	Leu	Val	Val	Thr	Lys	Gly	Asp
	290					295					300				
Gln	Tyr	Asp	Val	Arg	Glu	Gln	Ser	Asn	Glu	Asn	Glu	Val	Arg	Asn	Leu
305					310					315					320
Gly	Lys	Pro	Val	Asp	Leu	Ala	Gly	Gln	Tyr	Tyr	Lys	Asp	Gly	Ala	Asp
				325					330					335	

Glu Ile Ser Phe Leu Asn Ile Thr Gly Phe Arg Asp Phe Pro Leu Gly
 340 345 350
 Asp Leu Pro Met Ile Gln Val Leu Arg Gln Thr Ser Lys Asn Val Phe
 355 360 365
 Val Pro Leu Thr Val Gly Gly Gly Ile Arg Asp Phe Thr Asp Ala Ser
 370 375 380
 Gly Arg Tyr Tyr Ser Ser Leu Glu Val Ala Ala Glu Tyr Phe Arg Ser
 385 390 395 400
 Gly Ala Asp Lys Met Ser Ile Gly Ser Asp Ala Val Phe Ala Ala Glu
 405 410 415
 Glu Phe Ile Lys Ser Gly Val Lys Thr Gly Lys Ser Ser Leu Glu Gln
 420 425 430
 Ile Ser Arg Val Tyr Gly Asn Gln Ala Val Val Val Ser Ile Asp Pro
 435 440 445
 Arg Arg Val Tyr Val Asn His Pro Asp Asp Val Pro Tyr Lys Val Ile
 450 455 460
 Arg Val Thr Asn Pro Gly Pro Asn Gly Glu Glu Tyr Ala Trp Tyr Gln
 465 470 475 480
 Cys Thr Val Ser Gly Gly Gln Glu Gly Arg Pro Ile Gly Ala Phe Glu
 485 490 495
 Leu Ala Lys Ala Val Glu Glu Leu Gly Ala Gly Glu Ile Leu Leu Asn
 500 505 510
 Cys Ile Asn Cys Asp Gly Gln Gly Lys Gly Phe Asp Ile Asp Leu Val
 515 520 525
 Lys Leu Ile Ser Asp Ser Val Gly Ile Pro Val Ile Ala Ser Ser Gly
 530 535 540
 Ala Gly Thr Pro Asp His Phe Ser Glu Val Phe Glu Glu Asp Lys Arg
 545 550 555 560
 Ile Cys Arg Ala Cys Cys Arg His Phe Pro Pro Glu Arg Gly Tyr Gln
 565 570 575
 Ser Gln Ser Val Lys Glu His Leu Gln Glu Glu Arg Ile Glu Val Arg
 580 585 590
 Ile